FEB 0 5 2002

SEQUENCE LISTING

- PABO, Carl O.
- <120> DIMERIZING PEPTIDES
- <130> 8325-1004 / M4-US1

<110> WANG, Bryan S.

- <140> 09/636,243 <141> 2000-08-10
- <150> 60/148,422
- <151> 1999-08-11
- <160> 83
- <210> 1
- <211> 18
- <212> PRT
- <213> Artificial Sequence

<170> PatentIn Ver. 2.0

- <223> Description of Artificial Sequence: exemplary
- <220>
- <221> REPEAT <222> (2)
- <222> (2) <223> where 2-4 Xaa's are present

motif characterizing C2H2 class proteins

- <220> <221> REPEAT
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- <223> where 3-5 Xaa's are present
- <221> SITE <222> (2) <223> where Xaa is any amino acid
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1
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Xaa His
<210> 2
<211> 4
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<223> Description of Artificial Sequence: D-able
     subsite
<400> 2
Asn Asn Gly Lys
 1
<210> 3
<211> 9
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: zinc finger
     protein bind sequence
<400> 3
ggcgtagac
                                                             9
<210> 4
<211> 9
<212> DNA
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<223> Description of Artificial Sequence: zinc finger
     protein bind sequence
<400> 4
ggcgacgta
                                                             9
<210> 5
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     linker
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<400> 5
Thr Gly Glu Lys Pro
<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence
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Gly Gly Gly Ser
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<210> 7
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Gly Gly Arg Arg Gly Gly Ser
<210> 8
<211> 9
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Leu Arg Gln Arg Asp Gly Glu Arg Pro
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<211> 12
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1 5 10

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Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Ser Glu Arg Pro
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     finger of zinc finger protein
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4

Xaa His

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     domain F1
<400> 12
Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp
Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
<210> 13
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Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu
Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro
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ggttgcagtg ggcgcgccca cagtacttga acgtaacg
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<210> <211> <212> <213>	12	
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<400> tgggc	16 gtatg ct	12
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<400> agcat	17 acgcc ca	12
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<400> ggaat	18 teetg atcaagatet ggteaegtee ataggetagg catgteaagg etgtatg	57
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tgggcgcgcc ca
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atgggcgcgc ccat
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His Pro Met Asn Asn Leu Leu Asn Tyr Val Val Pro Lys Met Arg
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<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: DNA site used
      for affinity selection
<400> 23
gcagtgggcg cgcccacagt acttgaacgt aacg
                                                                  34
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<211> 15
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Gly Gly Gln Trp Leu Gly Thr Trp Glu Trp Tyr Gly Pro Lys
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<211> 15
<212> PRT
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Tyr Glu Lys Ile Ser Val Glu Gly Ile Lys Asp Val Arg Val Arg
<210> 26
<211> 15
<212> PRT
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Asn Val Ser Ile Glu Gly Val Leu Lys Tyr Tyr Arg Gly Leu Arg
                                     10
<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: peptide 4
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<400> 27

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Arg Ser Cys Gly Leu Asp Tyr Glu Gly Tyr Trp Leu Lys Leu Lys
 1
                  5
                                     10
<210> 28
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<212> PRT
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Ser Arg Trp Leu Glu Glu Glu Val Ser Arg Leu Leu Leu Arg
  1
                  5
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Gly Glu Ala Leu Asp Arg Phe Glu Arg Glu Met Lys Leu Met Arg
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Gly Gly Gln Trp
1
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<211> 5
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<223> Description of Artificial Sequence: sequential
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His Pro Met Asn Asn
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<212> PRT
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Pro Pro Ser Thr Glu
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Gln Lys Tyr Gly Asp
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Glu Asn Tyr Glu Lys
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Leu Leu Asn Tyr Lys
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Leu Leu Asn Tyr Val
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Leu Leu Asp Tyr Ile
 1
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block reoptimization sequence

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Leu Leu Asn Tyr Ile
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Leu Leu Gln Tyr Val
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Leu Leu Glu Tyr Lys
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Leu Leu Asp Tyr Val
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Leu Leu Asn Tyr Val
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Trp Tyr Gly Pro Lys
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His Pro Lys Met Lys
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<210> 46
<211> 5
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Pro Ala Lys Ile Arg
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<211> 5
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Val Pro Lys Ser Arg
  1
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<211> 5
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<400> 48
Val Pro Arg Leu Lys
<210> 49
<211> 5
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Ala Pro Lys Leu Arg
 1
                  5
<210> 50
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His Ala Lys Ile Arg
<210> 51
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210/ 31

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Val Val Lys Met Arg
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Pro Val Lys Met Arg
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<211> 5
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Val Pro Lys Gln Arg
 1
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Val Pro Lys Met Arg
  1
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Val Arg Lys Leu Arg
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Ser Arg Trp Leu Glu
 1
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Phe Arg Trp Leu Glu
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Gln Pro Trp Leu Thr
  1
                  5
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<211> 5
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Pro Pro Trp Leu Ile
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Pro Ala Trp Leu Thr
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Pro Ala Trp Leu Ala
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1 5

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Trp Ala Trp Leu Asp
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Pro Thr Trp Leu Thr
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Glu Glu Val Ser Arg
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Glu Tyr Leu Glu Ser
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Asp Tyr Val Thr Gln
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Asp Tyr Leu Ala Asp
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block reoptimization sequence

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Ser Tyr Leu Asp Lys
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Glu Tyr Met Ser Asp
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Met Arg Gly Trp Lys
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Met Gly Val Met Arg
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Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
Asp Glu Leu Thr Arg His Ile Arg Ile His Thr
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Glu Thr Asp Cys Arg Trp Asp Gly Cys Ser Gln Glu Phe Asp Ser Gln
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                                     10
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Glu Gln Leu Val His His Ile Asn Ser Glu His Ile

20 25

<210> 83

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<400> 83

Thr Phe Glu Cys Leu Phe Pro Gly Cys Thr Lys Thr Phe Lys Arg Arg 1 5 10 15

Tyr Asn Ile Arg Ser His Ile Gln Thr His Leu 20 25